

## **RAW SEQUENCE LISTING**

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Application Serial Number: 10/570,554  
Source: IFWP  
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IFWP

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/570,554

DATE: 03/15/2006

TIME: 12:18:40

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1 <110> APPLICANT: Broekaert, Willem
2      Frankard, Valerie
3      Hatzfeld, Yves
4      Mironov, Vladimir
5 <120> TITLE OF INVENTION: Plants having modified growth characteristics and method for
6      making the same
7 <130> FILE REFERENCE: 1187-44
8 <140> CURRENT APPLICATION NUMBER: US/10/570,554
9 <141> CURRENT FILING DATE: 2006-03-03
10 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/052035
11 <151> PRIOR FILING DATE: 2004-09-03
12 <150> PRIOR APPLICATION NUMBER: EP 03077811.2
13 <151> PRIOR FILING DATE: 2003-09-05
14 <160> NUMBER OF SEQ ID NOS: 21
15 <170> SOFTWARE: PatentIn version 3.3
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18 <211> LENGTH: 930
19 <212> TYPE: DNA
20 <213> ORGANISM: Arabidopsis thaliana
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24      gaagaaggta ttccaccaac tgctcttcgt gagatctcgc ttctccagat gttatcaaca      180
25      tcgatctatg ttgttcgatt actctgcgtc gaacatgttc atcaaccatc aaccaaattct      240
26      caatctacca aatccaatct ctatctcgtt ttcgagtatc tcgatactga tcttaagaaa      300
27      ttcatcgatt cgtataggaa aggacctaat cctaagcctc ttgagccttt tttgattcag      360
28      aagttgatgt ttcagctttg taaagggtgt gcgcattgtc atagtcattg tgtgcttcac      420
29      cgtgatctta aaccgcagaa tcttcttctg gtgaaagata aagagcttct taagattgct      480
30      gatttggtgc ttggtcgtgc ttttactggt cctcttaagt cttatacgca tgagattggt      540
31      actctttggt atagagctcc tgaagttctt cttggatcta ctcatattc aactggtggt      600
32      gacatgtggt ctggttggtg tatctttgct gagatgggtc ggaggcaagc tcttttcctt      660
33      ggtgattctg agtttcagca attgcttcat atcttcaggt tgctaggaac accaactgag      720
34      cagcaatggc cgggtgtttc cacactgcgt gactggcatg tttaccctaa gtgggagccg      780
35      caagacttaa ctcttgctgt tccttctctt tcacctcaag gagttgatct tctcacgaaa      840
36      atgctcaagt acaatccagc cgaaagaatt tcagcaaaaa cagcacttga tcacccatat      900
37      tttgacagcc ttgacaagtc tcagttctga      930
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40 <211> LENGTH: 309
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42 <213> ORGANISM: Arabidopsis thaliana
43 <400> SEQUENCE: 2
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46   Lys Val Tyr Lys Ala Met Glu Lys Gly Thr Gly Lys Leu Val Ala Leu
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48   Lys Lys Thr Arg Leu Glu Met Asp Glu Glu Gly Ile Pro Pro Thr Ala
49           35                      40                      45
50   Leu Arg Glu Ile Ser Leu Leu Gln Met Leu Ser Thr Ser Ile Tyr Val
51           50                      55                      60
52   Val Arg Leu Leu Cys Val Glu His Val His Gln Pro Ser Thr Lys Ser
53           65                      70                      75                      80
54   Gln Ser Thr Lys Ser Asn Leu Tyr Leu Val Phe Glu Tyr Leu Asp Thr
55           85                      90                      95
56   Asp Leu Lys Lys Phe Ile Asp Ser Tyr Arg Lys Gly Pro Asn Pro Lys
57           100                     105                     110
58   Pro Leu Glu Pro Phe Leu Ile Gln Lys Leu Met Phe Gln Leu Cys Lys
59           115                     120                     125
60   Gly Val Ala His Cys His Ser His Gly Val Leu His Arg Asp Leu Lys
61           130                     135                     140
62   Pro Gln Asn Leu Leu Leu Val Lys Asp Lys Glu Leu Leu Lys Ile Ala
63           145                     150                     155                     160
64   Asp Leu Gly Leu Gly Arg Ala Phe Thr Val Pro Leu Lys Ser Tyr Thr
65           165                     170                     175
66   His Glu Ile Val Thr Leu Trp Tyr Arg Ala Pro Glu Val Leu Leu Gly
67           180                     185                     190
68   Ser Thr His Tyr Ser Thr Gly Val Asp Met Trp Ser Val Gly Cys Ile
69           195                     200                     205
70   Phe Ala Glu Met Val Arg Arg Gln Ala Leu Phe Pro Gly Asp Ser Glu
71           210                     215                     220
72   Phe Gln Gln Leu Leu His Ile Phe Arg Leu Leu Gly Thr Pro Thr Glu
73           225                     230                     235                     240
74   Gln Gln Trp Pro Gly Val Ser Thr Leu Arg Asp Trp His Val Tyr Pro
75           245                     250                     255
76   Lys Trp Glu Pro Gln Asp Leu Thr Leu Ala Val Pro Ser Leu Ser Pro
77           260                     265                     270
78   Gln Gly Val Asp Leu Leu Thr Lys Met Leu Lys Tyr Asn Pro Ala Glu
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92   gaagaaggta taccaccaac ggctctccgt gagatctctc ttctccaaat gctttctcaa      180
93   tcaatctaca tcgttcgtct cctctgcgtc gaacatgtta ttcaatcgaa agattcgact      240
94   gtttctcact ctcccaaatc caatctctat ctcgtttttg agtatctcga cactgatctc      300
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98      attgctgatt tgggtcttag tcgtgctttt actgtgcctc ttaaggctta tacacatgag      540
99      attgttactc tttggtatag agctcctgaa gttttgcttg gttctactca ttactctact      600
100     gctgttgata tttggtctgt tggatgcac tttgccgaga tgattaggag gcaagctctt      660
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102     actgagcagc aatggccggg tgtaatggca ttgcgtgact ggcatgtcta tccaaagtgg      780
103     gagccgcaag acttatcacg tgctgttcca tctctatctc ctgaaggaat tgatcttctc      840
104     acgcaaatgt tgaagtacaa tccagcagaa agaatttcag caaaagcagc tctcgatcat      900
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108 <211> LENGTH: 311
109 <212> TYPE: PRT
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111 <400> SEQUENCE: 4
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114     Lys Val Tyr Lys Ala Met Glu Lys Thr Thr Gly Lys Leu Val Ala Leu
115           20          25          30
116     Lys Lys Thr Arg Leu Glu Met Asp Glu Glu Gly Ile Pro Pro Thr Ala
117           35          40          45
118     Leu Arg Glu Ile Ser Leu Leu Gln Met Leu Ser Gln Ser Ile Tyr Ile
119           50          55          60
120     Val Arg Leu Leu Cys Val Glu His Val Ile Gln Ser Lys Asp Ser Thr
121           65          70          75          80
122     Val Ser His Ser Pro Lys Ser Asn Leu Tyr Leu Val Phe Glu Tyr Leu
123           85          90          95
124     Asp Thr Asp Leu Lys Lys Phe Ile Asp Ser His Arg Lys Gly Ser Asn
125           100         105         110
126     Pro Arg Pro Leu Glu Ala Ser Leu Val Gln Arg Phe Met Phe Gln Leu
127           115         120         125
128     Phe Lys Gly Val Ala His Cys His Ser His Gly Val Leu His Arg Asp
129           130         135         140
130     Leu Lys Pro Gln Asn Leu Leu Leu Asp Lys Asp Lys Gly Ile Leu Lys
131           145         150         155         160
132     Ile Ala Asp Leu Gly Leu Ser Arg Ala Phe Thr Val Pro Leu Lys Ala
133           165         170         175
134     Tyr Thr His Glu Ile Val Thr Leu Trp Tyr Arg Ala Pro Glu Val Leu
135           180         185         190
136     Leu Gly Ser Thr His Tyr Ser Thr Ala Val Asp Ile Trp Ser Val Gly
137           195         200         205
138     Cys Ile Phe Ala Glu Met Ile Arg Arg Gln Ala Leu Phe Pro Gly Asp
139           210         215         220
140     Ser Glu Phe Gln Gln Leu Leu His Ile Phe Arg Leu Leu Gly Thr Pro
141           225         230         235         240
142     Thr Glu Gln Gln Trp Pro Gly Val Met Ala Leu Arg Asp Trp His Val
143           245         250         255
144     Tyr Pro Lys Trp Glu Pro Gln Asp Leu Ser Arg Ala Val Pro Ser Leu
145           260         265         270

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146      Ser Pro Glu Gly Ile Asp Leu Leu Thr Gln Met Leu Lys Tyr Asn Pro
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148      Ala Glu Arg Ile Ser Ala Lys Ala Ala Leu Asp His Pro Tyr Phe Asp
149              290                      295                      300
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151      305                      310
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154 <211> LENGTH: 948
155 <212> TYPE: DNA
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160      atcgttgctt tgaagaagac gcgtctccat gaggatgaag aaggtgttcc tcccactact      180
161      cttcgcgaga tctctatctt gcgtatgctc gctcgtgac ctcacatcgt taggttgatg      240
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172      gatctcttat ctaaaatgct ggagtacgag ccagcaaaac gaatctcagc aaagaaagct      900
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176 <211> LENGTH: 315
177 <212> TYPE: PRT
178 <213> ORGANISM: Arabidopsis thaliana
179 <400> SEQUENCE: 6
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184      Ala Arg Glu Lys Ala Thr Gly Met Ile Val Ala Leu Lys Lys Thr Arg
185              35              40              45
186      Leu His Glu Asp Glu Glu Gly Val Pro Pro Thr Thr Leu Arg Glu Ile
187              50              55              60
188      Ser Ile Leu Arg Met Leu Ala Arg Asp Pro His Ile Val Arg Leu Met
189              65              70              75              80
190      Asp Val Lys Gln Gly Ile Asn Lys Glu Gly Lys Thr Val Leu Tyr Leu
191              85              90              95
192      Val Phe Glu Tyr Val Asp Thr Asp Leu Lys Lys Phe Ile Arg Ser Phe
193              100             105             110
194      Arg Gln Ala Gly Gln Asn Ile Pro Gln Asn Thr Val Lys Cys Leu Met
195              115             120             125
196      Tyr Gln Leu Cys Lys Gly Met Ala Phe Cys His Gly His Gly Val Leu

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197	130	135	140
198	His Arg Asp Leu Lys Pro His Asn Leu Leu Met	Asp Arg Lys Thr Met	
199	145	150	155
200	Thr Leu Lys Ile Ala Asp Leu Gly Leu Ala Arg	Ala Phe Thr Leu Pro	
201		165	170
202	Met Lys Lys Tyr Thr His Glu Ile Leu Thr Leu	Trp Tyr Arg Ala Pro	
203		180	185
204	Glu Val Leu Leu Gly Ala Thr His Tyr Ser Thr	Gly Val Asp Met Trp	
205		195	200
206	Ser Val Gly Cys Ile Phe Ala Glu Leu Val Thr	Lys Gln Ala Ile Phe	
207		210	215
208	Ala Gly Asp Ser Glu Leu Gln Gln Leu Leu Arg	Ile Phe Arg Leu Leu	
209		225	230
210	Gly Thr Pro Asn Glu Glu Val Trp Pro Gly Val	Ser Lys Leu Lys Asp	
211		245	250
212	Trp His Glu Tyr Pro Gln Trp Lys Pro Leu Ser	Leu Ser Thr Ala Val	
213		260	265
214	Pro Asn Leu Asp Glu Ala Gly Leu Asp Leu Leu	Ser Lys Met Leu Glu	
215		275	280
216	Tyr Glu Pro Ala Lys Arg Ile Ser Ala Lys Lys	Ala Met Glu His Pro	
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218	Tyr Phe Asp Asp Leu Pro Asp Lys Ser Ser Leu		
219		305	310
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228	gggggttaacc ctgatggagc agtacgagaa ggaggagaag	attgggggagg gcacgtacgg	180
229	ggtggtgtac agggcgcggg acaagggtcac caacgagacg	atcgcgctca agaagatccg	240
230	gcttgagcag gaggatgagg gcgtcccctc caccgcaatc	cgcgagatct cgctcctcaa	300
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232	atatcttgtc tttgagtatc tggatctgga cctaaagaag	ttcatggact cttgtccaga	420
233	gtttgcgaaa aaccccaact taattaagtc atatctctat	cagatactcc gcggcggtgc	480
234	ttactgtcat tctcatagag ttcttcatcg agatttgaaa	cctcagaatt tattgataga	540
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236	tgtccgcacg tttactcacg aggttgtaac cttgtggtat	agagctccag agatccttct	660
237	tggatcaagg cagtattcta caccagttga tatgtggtca	gttggttgta tctttgcaga	720
238	aatggtgaac cagaaaccac tgttccctgg tgattctgag	attgatgaat tatttaagat	780
239	attcagggtta ctaggaactc caaatgaaca aagttggcca	ggagttagct cattacctga	840
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